

WHAT IS CLAIMED IS:

1. A method of inhibiting HBV attachment to a hepatic cell the method comprising the step of exposing the cell to a recombinant urine derived protein, said recombinant urine derived protein being capable of binding to a purified HBV derived polypeptide.

2. The method of claim 1, wherein said purified HBV derived polypeptide is HBsAg preS1 protein or a portion thereof.

3. The method of claim 1, wherein said recombinant urine derived protein includes a polypeptide selected from the group consisting of:

- (a) at least 60 % homologous with SEQ ID NO:4 or portions thereof as determined using the Bestfit procedure of the DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the university of Wisconsin (gap creation penalty - 50, gap extension penalty - 3);
- (b) being encoded by a polynucleotide at least 60 % identical to SEQ ID NOs:1, 3, 5 or portions thereof as determined using the Bestfit procedure of the DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the university of Wisconsin (gap creation penalty - 50, gap extension penalty - 3); and
- (c) being encoded by a polynucleotide hybridizable with SEQ ID NO:3 or portions thereof at 68 °C in 6 x SSC, 1 % SDS, 5 x Denharts, 10 % dextran sulfate, 100 µg/ml salmon sperm DNA, and ³²p labeled probe and wash at 68 °C with 3 x SSC and 0.1 % SDS.

4. The method of claim 3, wherein said polypeptide is as set fourth in SEQ ID NO:4 or portions thereof.

5. The method of claim 3, wherein said polypeptide is capable of specifically binding HBV particles.

6. The method of claim 3, wherein said polypeptide is capable of specifically binding to HBsAg preS1 protein or a portion thereof.

7. The method of claim 3, wherein said polypeptide is capable of specifically binding to a polypeptide as set forth in SEQ ID NOs:8 or 9.

8. The method of claim 3, wherein said recombinant urine derived protein is characterized by at least one of the following:

- (a) at least one EGF like domain;
- (b) at least one transmembrane domain;
- (c) at least one site for attachment of a hydroxyl side chain;
- (d) a signal peptide;
- (e) an RGD attachment sequence;
- (f) at least one glycosylation site; and
- (g) at least one disulfide bond.